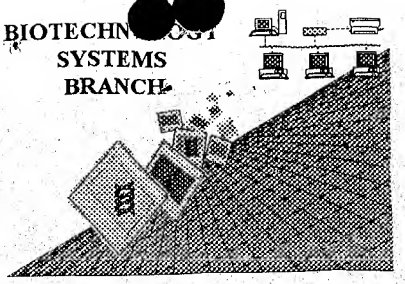
A: Nelson

File Copy 4117

BIOTECHNOLOGY SYSTEMS BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer-readable form:

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MAR 0 5 2001
TECH CENTER 1600/2900

Application Serial Number: 09/446,089A

Source: 1638

Date Processed by STIC: 2/27/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

http://www.uspto.gov/web/offices/pac/checker

Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION SERIAL NUMBER: 09/446,089A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

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1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 J Use of <220>Feature (NEW RULES)
Sequence(s) 10 are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

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1638

RAW SEQUENCE LISTING DATE: 02/27/2001
PATENT APPLICATION: US/09/446,089A TIME: 14:31:44

Input Set : A:\001560-377.ST25.txt
Output Set: N:\CRF3\02272001\I446089A.raw

p. 6

Does Not Comply
Corrected Diskette Needed

<110> APPLICANT: SAKAKIBARA, Keiko
FUKUI, Yuko
TANAKA, Yoshikazu
KUSUMI, Takaaki
MIZUTANI, Masako
NAKAYAMA, Toru
<120> TITLE OF INVENTION: GENE ENCODING PROTEIN HAVING AURONE SYNTHESIZING ACTIVITY
<130> FILE REFERENCE: 001560-377
<140> CURRENT APPLICATION NUMBER: US 09/446,089A
<141> CURRENT FILING DATE: 1999-12-17
<150> PRIOR APPLICATION NUMBER: PCT/JP99/02045
<151> PRIOR FILING DATE: 1999-04-16
<150> PRIOR APPLICATION NUMBER: JP 10/107296
<151> PRIOR FILING DATE: 1998-04-17
<160> NUMBER OF SEQ ID NOS: 15
<170> SOFTWARE: PatentIn version 3.0
<210> SEQ ID NO: 1
<211> LENGTH: 1951
<212> TYPE: DNA
<213> ORGANISM: Antirrhinum majus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (96)..(1781)
<400> SEQUENCE: 1

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gttgtttatt atcaatcaaa taaaattatt tccca atg ttc aaa aat cct aat         113
                                       Met Phe Lys Asn Pro Asn
                                       1               5
atc cgc tat cac aaa cta tct tcc aaa tcc aat gac aac gat caa gaa         161
Ile Arg Tyr His Lys Leu Ser Ser Lys Ser Asn Asp Asn Asp Gln Glu
            10                  15                  20
tcc tcc cat cgt tgt aag cac att cta tta ttt ata ata acc tta ttc         209
Ser Ser His Arg Cys Lys His Ile Leu Leu Phe Ile Ile Thr Leu Phe
        25                  30                  35
cta ctt ata gtt ggc ctg tac atc gcc aac tct ctc gcc tat gcc cgg         257
Leu Leu Ile Val Gly Leu Tyr Ile Ala Asn Ser Leu Ala Tyr Ala Arg
    40                  45                  50
ttt gcc tcg acc tca acc ggc cct atc gcc gcc cct gat gtc acc aaa         305
Phe Ala Ser Thr Ser Thr Gly Pro Ile Ala Ala Pro Asp Val Thr Lys
55                  60                  65                  70
tgt ggt cag cca gac ttg cca cct ggc aca gcc cca ata aac tgt tgt         353
Cys Gly Gln Pro Asp Leu Pro Pro Gly Thr Ala Pro Ile Asn Cys Cys
                75                  80                  85
ccc cca atc ccc gct aaa atc atc gat ttc gag cta cca cct ccc tcc         401
Pro Pro Ile Pro Ala Lys Ile Ile Asp Phe Glu Leu Pro Pro Pro Ser
            90                  95                  100
act acc atg agg gtt cgc cgt gcg gct cat tta gtt gat gat gca tac         449
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RAW SEQUENCE LISTING DATE: 02/27/2001
PATENT APPLICATION: US/09/446,089A TIME: 14:31:44

Input Set : A:\001560-377.ST25.txt
Output Set: N:\CRF3\02272001\I446089A.raw

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68 Thr Thr Met Arg Val Arg Arg Ala Ala His Leu Val Asp Asp Ala Tyr
69         105                 110                 115
71 att gcc aaa ttc aag aaa gcc gtt gag ctt atg cga gct cta cct gag      497
72 Ile Ala Lys Phe Lys Lys Ala Val Glu Leu Met Arg Ala Leu Pro Glu
73     120                 125                 130
75 gat gac cct cgt agc ttc aag caa caa gct aac gtc cat tgc gct tac      545
76 Asp Asp Pro Arg Ser Phe Lys Gln Gln Ala Asn Val His Cys Ala Tyr
77 135                 140                 145                 150
79 tgc gcg ggg gcg tat aat caa gcc ggt ttc aca aac cta aag ctc caa      593
80 Cys Ala Gly Ala Tyr Asn Gln Ala Gly Phe Thr Asn Leu Lys Leu Gln
81                 155                 160                 165
83 atc cac cga tct tgg ctt ttt ttc ccg ttc cat aga tat tat atc tac      641
84 Ile His Arg Ser Trp Leu Phe Phe Pro Phe His Arg Tyr Tyr Ile Tyr
85             170                 175                 180
87 ttt ttt gaa aga ata ttg gga aaa cta atc aat gat aca act ttt gct      689
88 Phe Phe Glu Arg Ile Leu Gly Lys Leu Ile Asn Asp Thr Thr Phe Ala
89         185                 190                 195
91 ctc caa ttt tgg aac tat gat tca cct ggt gga atg aca atc cca tca      737
92 Leu Gln Phe Trp Asn Tyr Asp Ser Pro Gly Gly Met Thr Ile Pro Ser
93     200                 205                 210
95 atg ttt att gat act aat tct tcg ctg tac gat agt tta cgg gac agt      785
96 Met Phe Ile Asp Thr Asn Ser Ser Leu Tyr Asp Ser Leu Arg Asp Ser
97 215                 220                 225                 230
99 aat cat cag cca cca acc atc gta gac ttg aac tac gcc ttt tct gat      833
100 Asn His Gln Pro Pro Thr Ile Val Asp Leu Asn Tyr Ala Phe Ser Asp
101                235                 240                 245
103 tcc gac aat acc act act cct gaa gag caa atg att ata aac ctt aaa      881
104 Ser Asp Asn Thr Thr Thr Pro Glu Glu Gln Met Ile Ile Asn Leu Lys
105            250                 255                 260
107 att gtg tac aga caa atg gtg tcg agc gct aag act cca cag ctt ttc      929
108 Ile Val Tyr Arg Gln Met Val Ser Ser Ala Lys Thr Pro Gln Leu Phe
109        265                 270                 275
111 ttc ggc cgc cca tac cga cgt ggg gac caa gag ttt ccc ggg gtg ggg      977
112 Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln Glu Phe Pro Gly Val Gly
113    280                 285                 290
115 tcg att gag tta gtc cct cat ggc atg ata cat tta tgg acc ggt tct     1025
116 Ser Ile Glu Leu Val Pro His Gly Met Ile His Leu Trp Thr Gly Ser
117 295                 300                 305                 310
119 gag aac acg ccc tat ggc gag aac atg ggg gct ttc tac tca acg gct     1073
120 Glu Asn Thr Pro Tyr Gly Glu Asn Met Gly Ala Phe Tyr Ser Thr Ala
121                315                 320                 325
123 aga gac ccg ata ttt ttt gct cat cat tcg aac gtc gat aga atg tgg     1121
124 Arg Asp Pro Ile Phe Phe Ala His His Ser Asn Val Asp Arg Met Trp
125            330                 335                 340
127 tcc ata tgg aag acc cta gga ggg ccg cgg agg acg gac tta aca gat     1169
128 Ser Ile Trp Lys Thr Leu Gly Gly Pro Arg Arg Thr Asp Leu Thr Asp
129        345                 350                 355
131 cca gat ttt ctt gat gcg tct ttc gtt ttt tat gac gaa aac gca gag     1217
132 Pro Asp Phe Leu Asp Ala Ser Phe Val Phe Tyr Asp Glu Asn Ala Glu
```

RAW SEQUENCE LISTING DATE: 02/27/2001
PATENT APPLICATION: US/09/446,089A TIME: 14:31:44

Input Set : A:\001560-377.ST25.txt
Output Set: N:\CRF3\02272001\I446089A.raw

```
133     360                 365                 370
135 atg gtt cgg gtc aag gtt cgg gat tgc tta gat gaa aag aaa cta ggg     1265
136 Met Val Arg Val Lys Val Arg Asp Cys Leu Asp Glu Lys Lys Leu Gly
137 375                 380                 385                 390
139 tac gtt tat caa gat gtg gag att ccg tgg ctc aac act cgt cca aca     1313
140 Tyr Val Tyr Gln Asp Val Glu Ile Pro Trp Leu Asn Thr Arg Pro Thr
141                 395                 400                 405
143 cca aaa gtt tct ccg tct cta ctt aag aaa ttt cat aga aca aac act     1361
144 Pro Lys Val Ser Pro Ser Leu Leu Lys Lys Phe His Arg Thr Asn Thr
145             410                 415                 420
147 gcc aat ccg aga caa gtt ttt cct gcg ata ctt gac aga gtc tta aaa     1409
148 Ala Asn Pro Arg Gln Val Phe Pro Ala Ile Leu Asp Arg Val Leu Lys
149         425                 430                 435
151 gtt atc gtg acg agg ccg aag aaa act aga agt agg aaa gaa aag gac     1457
152 Val Ile Val Thr Arg Pro Lys Lys Thr Arg Ser Arg Lys Glu Lys Asp
153     440                 445                 450
155 gag tta gaa gag att tta gtg att gaa ggg att gaa ctg gaa aga gac     1505
156 Glu Leu Glu Glu Ile Leu Val Ile Glu Gly Ile Glu Leu Glu Arg Asp
157 455                 460                 465                 470
159 cac ggg cac gta aaa ttc gac gtt tat att aat gct gac gaa gat gac     1553
160 His Gly His Val Lys Phe Asp Val Tyr Ile Asn Ala Asp Glu Asp Asp
161                 475                 480                 485
163 ctt gcg gtg att tcg ccg gag aat gct gag ttc gcc ggg agt ttc gtg     1601
164 Leu Ala Val Ile Ser Pro Glu Asn Ala Glu Phe Ala Gly Ser Phe Val
165             490                 495                 500
167 agt ctg tgg cac aaa cct ata aag ggg aag agg aca aag acg cag tta     1649
168 Ser Leu Trp His Lys Pro Ile Lys Gly Lys Arg Thr Lys Thr Gln Leu
169         505                 510                 515
171 tta aca ttg tcg att tgt gat att ttg gag gat ttg gat gct gac gaa     1697
172 Leu Thr Leu Ser Ile Cys Asp Ile Leu Glu Asp Leu Asp Ala Asp Glu
173     520                 525                 530
175 gat gat tat gtg ttg gtc act ttg gtt ccg aga aac gcc gga gat gcg     1745
176 Asp Asp Tyr Val Leu Val Thr Leu Val Pro Arg Asn Ala Gly Asp Ala
177 535                 540                 545                 550
179 atc aag att cat aat gtc aag att gag ctt gat ggc taataaattc          1791
180 Ile Lys Ile His Asn Val Lys Ile Glu Leu Asp Gly
181                 555                 560
183 tattgatttc ttctcaacct acagttgatc atttaccgat tgattattcc aataaaagta   1851
185 tctcatgtac caatatcgat cgtattaatc gtaatacttt cagattttta tttatttaaa   1911
187 agcagttgta taaatggtga aataaggatt actttttgag                         1951
190 <210> SEQ ID NO: 2
191 <211> LENGTH: 562
192 <212> TYPE: PRT
193 <213> ORGANISM: Antirrhinum majus
195 <400> SEQUENCE: 2
197 Met Phe Lys Asn Pro Asn Ile Arg Tyr His Lys Leu Ser Ser Lys Ser
198 1               5                   10                  15
201 Asn Asp Asn Asp Gln Glu Ser Ser His Arg Cys Lys His Ile Leu Leu
202             20                  25                  30
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RAW SEQUENCE LISTING DATE: 02/27/2001
PATENT APPLICATION: US/09/446,089A TIME: 14:31:44

Input Set : A:\001560-377.ST25.txt
Output Set: N:\CRF3\02272001\I446089A.raw

```
205 Phe Ile Ile Thr Leu Phe Leu Leu Ile Val Gly Leu Tyr Ile Ala Asn
206         35                  40                  45
209 Ser Leu Ala Tyr Ala Arg Phe Ala Ser Thr Ser Thr Gly Pro Ile Ala
210     50                  55                  60
213 Ala Pro Asp Val Thr Lys Cys Gly Gln Pro Asp Leu Pro Pro Gly Thr
214 65                  70                  75                  80
217 Ala Pro Ile Asn Cys Cys Pro Pro Ile Pro Ala Lys Ile Ile Asp Phe
218                 85                  90                  95
221 Glu Leu Pro Pro Pro Ser Thr Thr Met Arg Val Arg Arg Ala Ala His
222             100                 105                 110
225 Leu Val Asp Asp Ala Tyr Ile Ala Lys Phe Lys Lys Ala Val Glu Leu
226         115                 120                 125
229 Met Arg Ala Leu Pro Glu Asp Asp Pro Arg Ser Phe Lys Gln Gln Ala
230     130                 135                 140
233 Asn Val His Cys Ala Tyr Cys Ala Gly Ala Tyr Asn Gln Ala Gly Phe
234 145                 150                 155                 160
237 Thr Asn Leu Lys Leu Gln Ile His Arg Ser Trp Leu Phe Phe Pro Phe
238                 165                 170                 175
241 His Arg Tyr Tyr Ile Tyr Phe Phe Glu Arg Ile Leu Gly Lys Leu Ile
242             180                 185                 190
245 Asn Asp Thr Thr Phe Ala Leu Gln Phe Trp Asn Tyr Asp Ser Pro Gly
246         195                 200                 205
249 Gly Met Thr Ile Pro Ser Met Phe Ile Asp Thr Asn Ser Ser Leu Tyr
250     210                 215                 220
253 Asp Ser Leu Arg Asp Ser Asn His Gln Pro Pro Thr Ile Val Asp Leu
254 225                 230                 235                 240
257 Asn Tyr Ala Phe Ser Asp Ser Asp Asn Thr Thr Thr Pro Glu Glu Gln
258                 245                 250                 255
261 Met Ile Ile Asn Leu Lys Ile Val Tyr Arg Gln Met Val Ser Ser Ala
262             260                 265                 270
265 Lys Thr Pro Gln Leu Phe Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln
266         275                 280                 285
269 Glu Phe Pro Gly Val Gly Ser Ile Glu Leu Val Pro His Gly Met Ile
270     290                 295                 300
273 His Leu Trp Thr Gly Ser Glu Asn Thr Pro Tyr Gly Glu Asn Met Gly
274 305                 310                 315                 320
277 Ala Phe Tyr Ser Thr Ala Arg Asp Pro Ile Phe Phe Ala His His Ser
278                 325                 330                 335
281 Asn Val Asp Arg Met Trp Ser Ile Trp Lys Thr Leu Gly Gly Pro Arg
282             340                 345                 350
285 Arg Thr Asp Leu Thr Asp Pro Asp Phe Leu Asp Ala Ser Phe Val Phe
286         355                 360                 365
289 Tyr Asp Glu Asn Ala Glu Met Val Arg Val Lys Val Arg Asp Cys Leu
290     370                 375                 380
293 Asp Glu Lys Lys Leu Gly Tyr Val Tyr Gln Asp Val Glu Ile Pro Trp
294 385                 390                 395                 400
297 Leu Asn Thr Arg Pro Thr Pro Lys Val Ser Pro Ser Leu Leu Lys Lys
298                 405                 410                 415
301 Phe His Arg Thr Asn Thr Ala Asn Pro Arg Gln Val Phe Pro Ala Ile
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RAW SEQUENCE LISTING DATE: 02/27/2001
PATENT APPLICATION: US/09/446,089A TIME: 14:31:44

Input Set : A:\001560-377.ST25.txt
Output Set: N:\CRF3\02272001\I446089A.raw

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302                 420                 425                 430
305 Leu Asp Arg Val Leu Lys Val Ile Val Thr Arg Pro Lys Lys Thr Arg
306         435                 440                 445
309 Ser Arg Lys Glu Lys Asp Glu Leu Glu Glu Ile Leu Val Ile Glu Gly
310     450                 455                 460
313 Ile Glu Leu Glu Arg Asp His Gly His Val Lys Phe Asp Val Tyr Ile
314 465                 470                 475                 480
317 Asn Ala Asp Glu Asp Asp Leu Ala Val Ile Ser Pro Glu Asn Ala Glu
318                 485                 490                 495
321 Phe Ala Gly Ser Phe Val Ser Leu Trp His Lys Pro Ile Lys Gly Lys
322                 500                 505                 510
325 Arg Thr Lys Thr Gln Leu Leu Thr Leu Ser Ile Cys Asp Ile Leu Glu
326         515                 520                 525
329 Asp Leu Asp Ala Asp Glu Asp Asp Tyr Val Leu Val Thr Leu Val Pro
330     530                 535                 540
333 Arg Asn Ala Gly Asp Ala Ile Lys Ile His Asn Val Lys Ile Glu Leu
334 545                 550                 555                 560
337 Asp Gly
341 <210> SEQ ID NO: 3
342 <211> LENGTH: 13
343 <212> TYPE: PRT
344 <213> ORGANISM: Antirrhinum majus
346 <400> SEQUENCE: 3
348 Lys Lys Leu Gly Tyr Val Tyr Gln Asp Val Glu Ile Pro
349 1               5                   10
352 <210> SEQ ID NO: 4
353 <211> LENGTH: 12
354 <212> TYPE: PRT
355 <213> ORGANISM: Antirrhinum majus
357 <400> SEQUENCE: 4
359 Lys Ile Val Tyr Arg Gln Met Val Ser Ser Ala Lys
360 1               5                   10
362 <210> SEQ ID NO: 5
363 <211> LENGTH: 18
364 <212> TYPE: PRT
365 <213> ORGANISM: Antirrhinum majus
367 <400> SEQUENCE: 5
369 Lys Thr Pro Gln Leu Phe Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln
370 1               5                   10                  15
372 Glu Phe
375 <210> SEQ ID NO: 6
376 <211> LENGTH: 29
377 <212> TYPE: PRT
378 <213> ORGANISM: Antirrhinum majus
380 <220> FEATURE:
381 <221> NAME/KEY: UNSURE
382 <222> LOCATION: (9)..(9)
383 <223> OTHER INFORMATION: Amino acid 9 is Xaa wherein Xaa = unknown or other.
385 <220> FEATURE:
```

<210> 10
<211> 6
<212> PRT
<213> Artificial Sequence

See item 12 on Error Summary Sheet

<400> 10

His Ala Val Cys Asn Glu
1 5

FYI

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY DATE: 02/27/2001
PATENT APPLICATION: US/09/446,089A TIME: 14:31:45

Input Set : A:\001560-377.ST25.txt
Output Set: N:\CRF3\02272001\I446089A.raw

L:392 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:395 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:442 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:458 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:466 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:466 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:484 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:499 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:514 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13